system. Translational regulation was not observed when 5'-UTRs or 3'-UTRs alone were fused to the reporter gene. However, their simultaneous presence was sufficient to transfer differential translational control from the native transcript to the reporter transcript. This was true for both directions of translational control. Translational regulation was completely abolished when stem loops in the 5'-UTR were changed by mutagenesis. An "UTR-swap'' experiment demonstrated that the direction of translational regulation is encoded in the 3'-UTR, not in the 5'-UTR. While much is known about 5'-UTR-dependent translational control in bacteria, the reported findings provide the first examples that both 5'- and 3'-UTRs are essential and sufficient to drive differential translational regulation in a prokaryote and therefore have to functionally interact in vivo. The current results indicate that 3'-UTR-dependent translational control had already evolved before capping and polyadenylation of transcripts were invented, which are essential for circularization of transcripts in eukaryotes.

L10 ANSWER 2 OF 3 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
ACCESSION NUMBER: 2008:480895 BIOSIS
DOCUMENT NUMBER: PREV200800480894
TITLE: Step-wise formation of eukaryotic double-row polyribosomes and circular translation of polysomal mRNA.
AUTHOR(S): Kopeina, Gelina S.; Afonina, Zhanna A.; Gromova, Kira V.; Shirokov, Vladimir A.; Vasiliev, Victor D.; Spirin, Alexander S. [Reprint Author]
CORPORATE SOURCE: Russian Acad Sci, Inst Prot Res, Pushchino 142290, Moscow Region, Russia
spirin@vega.protres.ru
SOURCE: Nucleic Acids Research, (JUN 2008) Vol. 36, No. 8, pp. 2476-2488.
CODEN: NARHAD. ISSN: 0305-1048.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 3 Sep 2008
Last Updated on STN: 3 Sep 2008

AB The time course of polysome formation was studied in a long-term wheat germ cell-free translation system using sedimentation and electron microscopy techniques. The polysomes were formed on uncapped luciferase mRNA with translation-enhancing 5 and 3 UTRs. The formation of fully loaded polysomes was found to be a long process that required many rounds of translation and proceeded via several phases. First, short linear polysomes containing no more than six ribosomes were formed. Next, folding of these polysomes into short double-row clusters occurred. Subsequent gradual elongation of the clusters gave rise to heavy-loaded double-row strings containing up to 3040 ribosomes. The formation of the double-row polysomes was considered to be equivalent to circularization of polysomes, with antiparallel halves of the circle being laterally stuck together by ribosome interactions. A slow exchange with free ribosomes and free mRNA observed in the double-row type polysomes, as well as the resistance of translation in them to AMP-PNP, provided evidence that most polysomal ribosomes reinitiate translation within the circularized polysomes without scanning of 5 UTR, while de novo initiation including 5 UTR scanning proceeds at a much slower rate. Removal or replacements of 5 and 3 UTRs affected the initial phase of translation, but did not prevent the formation of the double-row polysomes during translation.

L10 ANSWER 3 OF 3 CAPLUS COPYRIGHT 2009 ACS on STN
ACCESSION NUMBER: 2007:648691 CAPLUS
DOCUMENT NUMBER: 147:339136
TITLE: Origin, evolution, and function of flavivirus RNA in untranslated and coding regions: implications for

virus transmission
AUTHOR(S): Gritsun, T. S.; Tuplin, A.; Gould, E. A.
CORPORATE SOURCE: Centre for Ecology and Hydrology, Oxford, UK
SOURCE: Molecular Biology of the Flavivirus (2006), 47-99.
Editor(s): Kalitzky, Matthias; Borowski, Peter.
Horizon Bioscience: Wymondham, UK.
CODEN: 69JHYP; ISBN: 978-1-904933-22-9
DOCUMENT TYPE: Conference; General Review
LANGUAGE: English

AB A review. In this review we analyze the research that specifically targets flavivirus RNA secondary structures. We focus mainly on data related to the 5' and 3' untranslated regions (5'UTR and 3'UTR) but the limited data relating to stable conserved secondary structures in the coding region of the flavivirus genome are also discussed. We propose that the 3'UTR, and possibly the open-reading frame, evolved through multiple duplication events of an RNA domain approx. 200 nucleotides in length, the remnants of which will be demonstrated in tick-borne flaviviruses. Subsequently, these repeat sequences and the associated RNA secondary structures may have evolved into stem-loop conformations with promoter and enhancer functions that impact on virus replication efficiency. The viral promoter probably folds as a complex transitional flexible RNA structure consisting of a number of transient stems and loops conserved between all flaviviruses. One of the transient forms of the promoter is formed due to the phys. interaction between multiple complementary sequences in the 3'UTR, the 5'
UTR and the coding region resulting in genome circularization.
The folding of the 3'UTR, independently from the 5'UTR, revealed other transient promoter elements that might occur before or after circularization. These include a terminal 3' stable long hairpin (3'LSH) with an adjacent dumbbell-like structure DB1. The folding of the 5'UTR predicts the formation of a conserved terminal Y-shaped structure that is essential for virus infectivity and might contribute to the promoter function. The replication enhancer is located in the 3'UTR between the stop codon and the promoter. It contains repeated conserved sequences and secondary structures but it is more variable between different flaviviruses than the promoter. Although the enhancer function may not be essential for virus viability under exptl. conditions in the laboratory, it might play a significant role in nature where the rate of virus replication could be critical for virus transmission and dissemination between vertebrates and invertebrates. The conserved RNA elements predicted in the coding region of the flavivirus genome might also function to accelerate virus replication in the environment thereby enhancing the likelihood of virus survival.

OS.CITING REF COUNT: 5 THERE ARE 5 CAPLUS RECORDS THAT CITE THIS RECORD (5 CITINGS)
REFERENCE COUNT: 107 THERE ARE 107 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

=> d hist

(FILE 'HOME' ENTERED AT 16:04:04 ON 13 NOV 2009)

FILE 'MEDLINE, CAPLUS, BIOSIS' ENTERED AT 16:04:46 ON 13 NOV 2009
L1 0 S (3')(W)(UTR)(S)(5')(W)(UTR)(S)(VEGF)(S)(INTERACT?)
L2 0 S (3')(W)(UTR)(S)(5')(W)(UTR)(S)(VEGF) AND (INTERACT?)
L3 0 S (3')(W)(UTR) AND (5')(W)(UTR) AND (VEGF) AND (INTERACT?)
L4 0 S (3')(W)(UTR) AND (5')(W)(UTR) AND (INTERACT?)
L5 3 S (3' UTR) AND (5' UTR) AND (INTERACT?)
L6 0 S L5 AND "VEGF"
L7 46 S (UTR) AND (INTERACT?) AND ("VEGF")

```
L8             5 S L7 AND (5' AND 3')
L9             3 DUP REM L8 (2 DUPLICATES REMOVED)
L10            3 DUP REM L5 (0 DUPLICATES REMOVED)

=> d hist full

     (FILE 'HOME' ENTERED AT 16:04:04 ON 13 NOV 2009)

     FILE 'MEDLINE, CAPLUS, BIOSIS' ENTERED AT 16:04:46 ON 13 NOV 2009
L1             0 SEA ABB=ON  PLU=ON  (3')(W)(UTR)(S)(5')(W)(UTR)(S)(VEGF)(S)(INT
                 ERACT?)
L2             0 SEA ABB=ON  PLU=ON  (3')(W)(UTR)(S)(5')(W)(UTR)(S)(VEGF) AND
                 (INTERACT?)
L3             0 SEA ABB=ON  PLU=ON  (3')(W)(UTR) AND (5')(W)(UTR) AND (VEGF)
                 AND (INTERACT?)
L4             0 SEA ABB=ON  PLU=ON  (3')(W)(UTR) AND (5')(W)(UTR) AND (INTERACT
                 ?)
L5             3 SEA ABB=ON  PLU=ON  (3' UTR) AND (5' UTR) AND (INTERACT?)
L6             0 SEA ABB=ON  PLU=ON  L5 AND "VEGF"
L7            46 SEA ABB=ON  PLU=ON  (UTR) AND (INTERACT?) AND ("VEGF")
L8             5 SEA ABB=ON  PLU=ON  L7 AND (5' AND 3')
L9             3 DUP REM L8 (2 DUPLICATES REMOVED)
L10            3 DUP REM L5 (0 DUPLICATES REMOVED)
                 D L10 IBIB ABS 1-3


     FILE HOME

     FILE MEDLINE
      FILE LAST UPDATED: 11 Nov 2009 (20091111/UP).  FILE COVERS 1949 TO DATE.

      MEDLINE and LMEDLINE have been updated with the 2009 Medical Subject
      Headings (MeSH) vocabulary and tree numbers from the U.S.  National Libra
      of Medicine (NLM).  Additional information is available at

      http://www.nlm.nih.gov/pubs/techbull/nd08/nd08_medline_data_changes_2009.

      On February 21, 2009, MEDLINE was reloaded.  See HELP RLOAD for details.

      This file contains CAS Registry Numbers for easy and accurate
      substance identification.

      See HELP RANGE before carrying out any RANGE search.

     FILE CAPLUS

     Copyright of the articles to which records in this database refer is
     held by the publishers listed in the PUBLISHER (PB) field (available
     for records published or updated in Chemical Abstracts after December
     26, 1996), unless otherwise indicated in the original publications.
     The CA Lexicon is the copyrighted intellectual property of the
     American Chemical Society and is provided to assist you in searching
     databases on STN.  Any dissemination, distribution, copying, or storing
     of this information, without the prior written consent of CAS, is
     strictly prohibited.

     FILE COVERS 1907 - 13 Nov 2009  VOL 151 ISS 21
     FILE LAST UPDATED: 12 Nov 2009  (20091112/ED)
     REVISED CLASS FIELDS (/NCL) LAST RELOADED:  Aug 2009
     USPTO MANUAL OF CLASSIFICATIONS THESAURUS ISSUE DATE:  Aug 2009

     CAplus now includes complete International Patent Classification (IPC)
```